

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/589,594
Source: JFW/P
Date Processed by STIC: 8/28/06

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

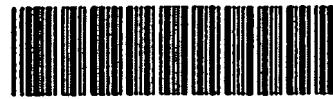
Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

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- 1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)**
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Revised 01/10/06



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/589,594

DATE: 08/28/2006
TIME: 10:43:27

Input Set : A:\082368-008900US.txt
Output Set: N:\CRF4\08282006\J589594.raw

4 <110> APPLICANT: Nakamura, Yusuke
5 Furukawa, Yoichi
7 <120> TITLE OF INVENTION: METHOD FOR DIAGNOSING COLORECTAL CANCERS
10 <130> FILE REFERENCE: 082368-008900US
!--> 12 <140> CURRENT APPLICATION NUMBER: US/10/589,594
!--> 12 <141> CURRENT FILING DATE: 2006-08-15
12 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/002145
13 <151> PRIOR FILING DATE: 2004-02-24
15 <160> NUMBER OF SEQ ID NOS: 23
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2624
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (294)...(1688)
28 <400> SEQUENCE: 1
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30 gcgaccgcgg agggtggcga gggggcgccca ggacccgcag cccccggggcc gggccgggtcc 120
31 ggacccgcag ggagggcagg tcagtggcga gatcgcgtcc gcgggattca atctctgccc 180
32 gctctgataa cagtccttt ccctggcgct cacttcgtgc ctggcacccg gctgggcgcc 240
33 tcaagaccgt tgctcttcg atcgcttctt tggacttggc gaccatttca gag atg 296
34 Met
35 1
37 tct tcc aga agt acc aaa gat tta att aaa agt aag tgg gga tcg aag 344
38 Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys
39 5 10 15
41 cct agt aac tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa 392
42 Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu
43 20 25 30
45 att gca cac tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga 440
46 Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly
47 35 40 45
49 aag ctg act gat aaa gag aga cac aga ctt ttg gag aaa att cga gtc 488
50 Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg Val
51 50 55 60 65
53 ctt gag gct gag aag gag aat gct tat caa ctc aca gag aag gac 536
54 Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys Asp
55 70 75 80
57 aaa gaa ata cag cga ctg aga gac caa ctg aag gcc aga tat agt act 584
58 Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr
59 85 90 95

See p. 8
**Does Not Comply
Corrected Diskette Needed**

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/589,594

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Input Set : A:\082368-008900US.txt
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61	acc	gca	ttg	ctt	gaa	cag	ctg	gaa	gag	aca	acg	aga	gaa	gga	gaa	agg		632
62	Thr	Ala	Leu	Leu	Glu	Gln	Leu	Glu	Glu	Thr	Thr	Arg	Glu	Gly	Glu	Arg		
63	100				105					110								
65	agg	gag	cag	gtg	ttg	aaa	gcc	tta	tct	gaa	gag	aaa	gac	gta	ttg	aaa		680
66	Arg	Glu	Gln	Val	Leu	Lys	Ala	Leu	Ser	Glu	Glu	Lys	Asp	Val	Leu	Lys		
67	115				120					125								
69	caa	cag	ttg	tct	gct	gca	acc	tca	cga	att	gct	gaa	ctt	gaa	agc	aaa		728
70	Gln	Gln	Leu	Ser	Ala	Ala	Thr	Ser	Arg	Ile	Ala	Glu	Leu	Glu	Ser	Lys		
71	130				135					140								145
73	acc	aat	aca	ctc	cgt	tta	tca	cag	act	gtg	gct	cca	aac	tgc	ttc	aac		776
74	Thr	Asn	Thr	Leu	Arg	Leu	Ser	Gln	Thr	Val	Ala	Pro	Asn	Cys	Phe	Asn		
75	150				155					160								
77	tca	tca	ata	aat	aat	att	cat	gaa	atg	gaa	ata	cag	ctg	aaa	gat	gct		824
78	Ser	Ser	Ile	Asn	Asn	Ile	His	Glu	Met	Glu	Ile	Gln	Leu	Lys	Asp	Ala		
79	165				170					175								
81	ctg	gag	aaa	aat	cag	cag	tgg	ctc	gtg	tat	gat	cag	cag	cg	gaa	gtc		872
82	Leu	Glu	Lys	Asn	Gln	Gln	Trp	Leu	Val	Tyr	Asp	Gln	Gln	Arg	Glu	Val		
83	180				185					190								
85	tat	gta	aaa	gga	ctt	tta	gca	aag	atc	ttt	gag	ttg	gaa	aag	aaa	acg		920
86	Tyr	Val	Lys	Gly	Leu	Leu	Ala	Lys	Ile	Phe	Glu	Leu	Glu	Lys	Thr			
87	195				200					205								
89	gaa	aca	gct	gct	cat	tca	ctc	cca	cag	cag	aca	aaa	aag	cct	gaa	tca		968
90	Glu	Thr	Ala	Ala	His	Ser	Leu	Pro	Gln	Gln	Thr	Lys	Lys	Pro	Glu	Ser		
91	210				215					220								225
93	gaa	ggt	tat	ctt	caa	gaa	gag	cag	aaa	tgt	tac	aac	gat	ctc	ttg		1016	
94	Glu	Gly	Tyr	Leu	Gln	Glu	Glu	Lys	Gln	Lys	Cys	Tyr	Asn	Asp	Leu	Leu		
95	230				235					240								
97	gca	agt	gca	aaa	aaa	gat	ctt	gag	gtt	gaa	cga	caa	acc	ata	act	cag		1064
98	Ala	Ser	Ala	Lys	Lys	Asp	Leu	Glu	Val	Glu	Arg	Gln	Thr	Ile	Thr	Gln		
99	245				250					255								
101	ctg	agt	ttt	gaa	ctg	agt	gaa	ttt	cga	aga	aaa	tat	gaa	gaa	acc	caa		1112
102	Leu	Ser	Phe	Glu	Leu	Ser	Glu	Phe	Arg	Arg	Lys	Tyr	Glu	Glu	Thr	Gln		
103	260				265					270								
105	aaa	gaa	gtt	cac	aat	tta	aat	cag	ctg	ttg	tat	tca	caa	aga	agg	gca		1160
106	Lys	Glu	Val	His	Asn	Leu	Asn	Gln	Leu	Leu	Tyr	Ser	Gln	Arg	Arg	Ala		
107	275				280					285								
109	gat	gtg	caa	cat	ctg	gaa	gat	gat	agg	cat	aaa	aca	gag	aag	ata	caa		1208
110	Asp	Val	Gln	His	Leu	Glu	Asp	Asp	Arg	His	Lys	Thr	Glu	Lys	Ile	Gln		
111	290				295					300								305
113	aaa	ctc	agg	gaa	gag	aat	gat	att	gct	agg	gga	aaa	ctt	gaa	gag		1256	
114	Lys	Leu	Arg	Glu	Glu	Asn	Asp	Ile	Ala	Arg	Gly	Lys	Leu	Glu	Glu			
115	310				315					320								
117	aag	aag	aga	tcc	gaa	gag	ctc	tta	tct	cag	gtc	cag	ttt	ctt	tac	aca		1304
118	Lys	Lys	Arg	Ser	Glu	Glu	Leu	Leu	Ser	Gln	Val	Gln	Phe	Leu	Tyr	Thr		
119	325				330					335								
121	tct	ctg	cta	aag	cag	caa	gaa	caa	aca	agg	gta	gct	ctg	ttg	gaa		1352	
122	Ser	Leu	Leu	Lys	Gln	Gln	Glu	Glu	Gln	Thr	Arg	Val	Ala	Leu	Leu	Glu		
123	340				345					350								
125	caa	cag	atg	cag	gca	tgt	act	tta	gac	ttt	gaa	aat	gaa	aaa	ctc	gac		1400

RAW SEQUENCE LISTING
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126	Gln	Met	Gln	Ala	Cys	Thr	Leu	Asp	Phe	Glu	Asn	Glu	Lys	Leu	Asp		
127	355					360				365							
129	cgt	caa	cat	gtg	cag	cat	caa	ttg	cat	gta	att	ctt	aag	gag	ctc	cga	1448
130	Arg	Gln	His	Val	Gln	His	Gln	Leu	His	Val	Ile	Leu	Lys	Glu	Leu	Arg	
131	370					375				380			385				
133	aaa	gca	aga	aat	caa	ata	aca	cag	ttg	gaa	tcc	ttg	aaa	cag	ctt	cat	1496
134	Lys	Ala	Arg	Asn	Gln	Ile	Thr	Gln	Leu	Glu	Ser	Leu	Lys	Gln	Leu	His	
135						390				395			400				
137	gag	ttt	gcc	atc	aca	gag	cca	tta	gtc	act	ttc	caa	gga	gag	act	gaa	1544
138	Glu	Phe	Ala	Ile	Thr	Glu	Pro	Leu	Val	Thr	Phe	Gln	Gly	Glu	Thr	Glu	
139						405				410			415				
141	aac	aga	gaa	aaa	gtt	gcc	gcc	tca	cca	aaa	agt	ccc	act	gct	gca	ctc	1592
142	Asn	Arg	Glu	Lys	Val	Ala	Ala	Ser	Pro	Lys	Ser	Pro	Thr	Ala	Ala	Leu	
143						420				425			430				
145	aat	gaa	agc	ctg	gtg	gaa	tgt	ccc	aag	tgc	aat	ata	cag	tat	cca	gcc	1640
146	Asn	Glu	Ser	Leu	Val	Glu	Cys	Pro	Lys	Cys	Asn	Ile	Gln	Tyr	Pro	Ala	
147						435				440			445				
149	act	gag	cat	cgc	gat	ctg	ctt	gtc	cat	gtg	gaa	tac	tgt	tca	aag	tag	1688
150	Thr	Glu	His	Arg	Asp	Leu	Leu	Val	His	Val	Glu	Tyr	Cys	Ser	Lys	*	
151	450						455				460						
153	caaaaataagt	atttggtttg	atattaaaag	attcaatact	gtat	tttctg	tttagctt	gtgtgt	tttagctt	gtat	ttttttttt	ttttttttt	ttttttttt	ttttttttt	ttttttttt	ttttttttt	1748
154	ggcattttga	atttatattt	tcacattttg	cataaaactg	cctatctacc	tttgacactc	1808										
155	cagcatgcta	gtgaatcatg	tatcttttag	gctgtgtgc	attttcttgc	gcagtgtatc	1868										
156	ctccctgaca	tggttcatca	tcaggctgca	atgacagaat	gtggtagca	gcgtctactg	1928										
157	agactactaa	catttgcac	tgtcaaaata	cttggtaggg	aaaagatagc	tcaggttatt	1988										
158	gctaatgggt	taatgcacca	gcaagcaaaa	tattttatgt	tttgggggtt	tgaaaaatca	2048										
159	aagataatta	accaaggatc	ttaactgtgt	tcgcattttt	tatccaagca	cttagaaaaac	2108										
160	ctacaatcct	aattttgtat	tccattgtta	agaggtgtgt	atagatacta	ttttttttttt	2168										
161	catattgtat	agcggttatt	agaaaaagttt	gggattttct	tgatctttat	tgctgtttac	2228										
162	cattgaaact	taacccttgt	gtgtccccca	actctgttct	gcccacacaca	cagtatctgt	2288										
163	ttgaggcata	atcttaagtg	gccacacacaca	atgttttctc	ttatgttattc	ttggcagtaac	2348										
164	tgttaacttgc	attacatttag	cacattctgc	ttagctaaaa	ttgtttaaaaat	aaactttaat	2408										
165	aaacccatgt	agccctctca	tttgatttgc	agtattttag	ttat	ttttttttttt	2468										
166	gctgggcaat	gtaatgtca	gatctttgtt	tgtctgaaca	ggtattttta	tacatgttt	2528										
167	ttgttaaacca	aaaacttttta	aattttttca	ggttttctaa	catgcttacc	actgggttac	2588										
168	tgttaaatgtat	aaaagaataaa	aatttttttaa	tgtttt													2624
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171	<211>	LENGTH:	464														
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173	<213>	ORGANISM:	Homo sapiens														
175	<400>	SEQUENCE:	2														
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177	1					5				10				15			
178	Lys	Pro	Ser	Asn	Ser	Lys	Ser	Glu	Thr	Thr	Leu	Glu	Lys	Leu	Lys	Gly	
179						20				25			30				
180	Glu	Ile	Ala	His	Leu	Lys	Thr	Ser	Val	Asp	Glu	Ile	Thr	Ser	Gly	Lys	
181						35				40			45				
182	Gly	Lys	Leu	Thr	Asp	Lys	Glu	Arg	His	Arg	Leu	Leu	Glu	Lys	Ile	Arg	
183						50				55			60				

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Input Set : A:\082368-008900US.txt
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184 Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys
 185 65 70 75 80
 186 Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser
 187 85 90 95
 188 Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu
 189 100 105 110
 190 Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu
 191 115 120 125
 192 Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser
 193 130 135 140
 194 Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe
 195 145 150 155 160
 196 Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp
 197 165 170 175
 198 Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu
 199 180 185 190
 200 Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys
 201 195 200 205
 202 Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu
 203 210 215 220
 204 Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu
 205 225 230 235 240
 206 Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr
 207 245 250 255
 208 Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr
 209 260 265 270
 210 Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg
 211 275 280 285
 212 Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile
 213 290 295 300
 214 Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu
 215 305 310 315 320
 216 Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr
 217 325 330 335
 218 Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu
 219 340 345 350
 220 Glu Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu
 221 355 360 365
 222 Asp Arg Gln His Val Gln His Val Ile Leu Lys Glu Leu
 223 370 375 380
 224 Arg Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu
 225 385 390 395 400
 226 His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr
 227 405 410 415
 228 Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala
 229 420 425 430
 230 Leu Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro
 231 435 440 445
 232 Ala Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys

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Input Set : A:\082368-008900US.txt
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233	450	455	460
236	<210> SEQ ID NO: 3		
237	<211> LENGTH: 22		
238	<212> TYPE: DNA		
239	<213> ORGANISM: Artificial Sequence		
241	<220> FEATURE:		
242	<223> OTHER INFORMATION: An artificially synthesized primer sequence for		
243	RT-PCR		
245	<400> SEQUENCE: 3		
246	acaacagcct caagatcatc ag		22
248	<210> SEQ ID NO: 4		
249	<211> LENGTH: 20		
250	<212> TYPE: DNA		
251	<213> ORGANISM: Artificial Sequence		
253	<220> FEATURE:		
254	<223> OTHER INFORMATION: An artificially synthesized primer sequence for		
255	RT-PCR		
257	<400> SEQUENCE: 4		
258	ggtccaccac tgacacgttg		20
260	<210> SEQ ID NO: 5		
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262	<212> TYPE: DNA		
263	<213> ORGANISM: Artificial Sequence		
265	<220> FEATURE:		
266	<223> OTHER INFORMATION: An artificially synthesized primer sequence for		
267	RT-PCR		
269	<400> SEQUENCE: 5		
270	agagatccga agagcttta tct		23
272	<210> SEQ ID NO: 6		
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274	<212> TYPE: DNA		
275	<213> ORGANISM: Artificial Sequence		
277	<220> FEATURE:		
278	<223> OTHER INFORMATION: An artificially synthesized primer sequence for		
279	RT-PCR		
281	<400> SEQUENCE: 6		
282	gatgctcagt ggctggatac t		21
284	<210> SEQ ID NO: 7		
285	<211> LENGTH: 24		
286	<212> TYPE: DNA		
287	<213> ORGANISM: Artificial Sequence		
289	<220> FEATURE:		
290	<223> OTHER INFORMATION: An artificially synthesized primer sequence for		
291	RT-PCR		
293	<400> SEQUENCE: 7		
294	cgtaaagcttc agagatgtct tcca		24
296	<210> SEQ ID NO: 8		
297	<211> LENGTH: 27		
298	<212> TYPE: DNA		

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

se of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
& <223> fields of each sequence which presents at least one n or Xaa.

eq#:23; N Pos. 489,490,491,492

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/589,594

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Input Set : A:\082368-008900US.txt
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:12 M:270 C: Current Application Number differs, Replaced Current Application No
:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
:485 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
:489 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
:498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:480

10/589,594

8

<210> 23
<211> 5089
<212> DNA
<213> Artificial Sequence

<220>

<223> An artificially synthesized vector sequence

<221> misc_feature

<222> (489)...(492)

<223> n = GAP

<400> 23

"n" can only represent a single nucleotide, nothing
else